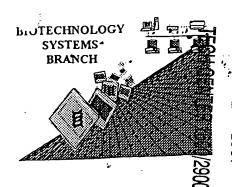
BEST AVAILABLE COPY

RAW SEQUENCE LISTING ERROR REPORT

361



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09596444

Date Processed by STIC: 10/24/

Source:

NGV 1 3 2001 C. T. O. P. 3600

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 c-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 c-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/596 444
ATTN: NEW RULES CASE	S: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use apace characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6Patentin 2.0 "bug"	A "bug" in Patentln version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, Patentln would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s)missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown c is Artificial Sequence.
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
Patentin 2.0 "bug"	Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13Misuse of n	in can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.
₹ · 	AMC/MH - Biotechnology Systems Branch - 0877172001 CEIVED

NOV 1 3 2001

GROUP 3600

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

DATE: 10/24/2001 TIME: 14:32:01

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                      Output Set: N:\CRF3\10242001\I596444.raw
      3 <110> APPLICANT: Huang, Wei
              Hoekstra, Merl F
      5
               Lee, Sandra K
                                                                        Does Not Comply
               Cairns, Nicholas
      6
               Kauvar, Lawrence M
      7
                                                                    Corrected Diskette Needed
               Sportsman, J Richard
     10 <120> TITLE OF INVENTION: PHOSPHORYLATION ASSAYS
     12 <130> FILE REFERENCE: LJL 354B
     14 <140> CURRENT APPLICATION NUMBER: US 09/596,444
                                    Errored: A 213 response of "Artificial"
223.

Gield 223.

requires ar explanation on the preferres

FYI: "Artificial Sequence" is the preferres

OSPHORYLATION response. Mit
     15 <141> CURRENT FILING DATE: 2000-06-19
     17 <160> NUMBER OF SEQ ID NOS: 48
     19 <170> SOFTWARE: PatentIn version 3.1
     21 <210> SEQ ID NO: 1
     22 <211> LENGTH: 10
     23 <212> TYPE: PRT
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     28 <222> LOCATION: (5)..(5)
     29 <223> OTHER INFORMATION: PHOSPHORYLATION
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     33 <221> NAME/KEY: MOD_RES
     34 <222> LOCATION: (10)..(10)
     35 <223> OTHER INFORMATION: BIOTINYLATION
     38 <400> SEOUENCE: 1
     40 Gly Glu Glu Gly Tyr Met Pro Met Gly Lys
     41 1
     44 <210> SEQ ID NO: 2
                                                   A field 223 esplanation to wardstory
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                                                                                    NOV 1 3 2001
     58 <223> OTHER INFORMATION: AMIDATION
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     61 <400> SEQUENCE: 2
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     64 1
                                               10
     67 Phe
     71 <210> SEQ ID NO: 3
     72 <211> LENGTH: 8
     73 <212> TYPE: PRT
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/596,444

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING DATE: 10/24/2001 PATENT APPLICATION: US/09/596,444 TIME: 14:32:01

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     78 Asp Tyr Met Thr Met Gln Ile Gly
     79 1
     82 <210> SEQ ID NO: 4
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     84 <212> TYPE: PRT
C--> 85 <213> ORGANISM: Artixicial
W--> 87 <220> FEATURE:
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     90 1
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W--> 98 <220> FEATURE:
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     135 1
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DATE: 10/24/2001

TIME: 14:32:01 PATENT APPLICATION: US/09/596,444 Input Set : A:\Sequence Listing.txt.txt Output Set: N:\CRF3\10242001\I596444.raw 143 <220> FEATURE: 144 <221> NAME/KEY: MOD_RES 145 <222> LOCATION: (5)..(5) 146 <223> OTHER INFORMATION: PHOSPHORYLATION 149 <220> FEATURE: 150 <221>, NAME/KEY: MOD_RES 151 <222> LOCATION: (7)..(7) 152 <223> OTHER INFORMATION: PHOSPHORYLATION 155 <400> SEQUENCE: 8 157 Glu Lys Arg Pro Ser Arg Ser Tyr Leu 158 1 161 <210> SEQ ID NO: 9 162 <211> LENGTH: 14 163 <212> TYPE: PRT C--> 164 <213> ORGANISM: Artificial 166 <220> FEATURE: 167 <221> NAME/KEY: MOD_RES 168 <222> LOCATION: (11)..(11) 169 <223> OTHER INFORMATION: PHOSPHORYLATION 172 <400> SEQUENCE: 9 174 Lys Arg Arg Glu Ile Leu Ser Arg Arg Pro Ser Tyr Arg Lys 175 1 10 178 <210> SEQ ID NO: 10 179 <211> LENGTH: 11 180 <212> TYPE: PRT C--> 181 <213 > ORGANISM: Artificial 183 <220> FEATURE: 184 <221> NAME/KEY: MOD_RES 185 <222> LOCATION: (7)..(7) 186 <223> OTHER INFORMATION: PHOSPHORYLATION 189 <400> SEQUENCE: 10 191 Lys His Phe Pro Gln Phe Ser Tyr Ser Ala Ser 192 1 195 <210> SEQ ID NO: 11 196 <211> LENGTH: 11 197 <212> TYPE: PRT C--> 198 <213> ORGANISM: Artificial 200 <220> FEATURE: 201 <221> NAME/KEY: MOD_RES 202 <222> LOCATION: (1)..(1) 203 <223> OTHER INFORMATION: PHOSPHORYLATION 206 <400> SEQUENCE: 11 208 Ser Pro Glu Leu Glu Arg Leu Ile Ile Gln Cys 212 <210> SEQ ID NO: 12

RAW SEQUENCE LISTING

213 <211> LENGTH: 11 214 <212> TYPE: PRT

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C--> 215 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING DATE: 10/24/2001 PATENT APPLICATION: US/09/596,444 TIME: 14:32:01

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Output Set: N:\CRF3\10242001\1596444.raw

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RAW SEQUENCE LISTING DATE: 10/24/2001 PATENT APPLICATION: US/09/596,444 TIME: 14:32:01 Input Set : A:\Sequence Listing.txt.txt Output Set: N:\CRF3\10242001\I596444.raw 293 <222> LOCATION: (4)..(4) 294 <223> OTHER INFORMATION: PHOSPHORYLATION 297 <400> SEQUENCE: 16 299 Arg Lys Arg Thr Leu Arg Arg Leu 303 <210> SEQ ID NO: 17 304 <211> LENGTH: 7 305 <212> TYPE: PRT C--> 306 <213> ORGANISM: Artificial 308 <220> FEATURE: 309 <221> NAME/KEY: MOD_RES 310 <222> LOCATION: (5)..(5) 311 <223> OTHER INFORMATION: PHOSPHORYLATION 314 <400> SEQUENCE: 17 316 Leu Arg Arg Ala Ser Leu Gly 317 1 320 <210> SEQ ID NO: 18 321 <211> LENGTH: 12 322 <212> TYPE: PRT

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365 <220> FEATURE:

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343 <221> NAME/KEY: MOD_RES 344 <222> LOCATION: (6)..(6)

349 <221> NAME/KEY: MOD_RES 350 <222> LOCATION: (7)..(7)

356 Arg Pro Arg Ala Ala Thr Phe

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328 <223> OTHER INFORMATION: PHOSPHORYLATION

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351 <223> OTHER INFORMATION: AMIDATION

333 Lys Lys Leu Asn Arg Thr Leu Ser Val Ala Ser Leu

325 <220> FEATURE:

 VERIFICATION SUMMARY
 DATE: 10/24/2001

 PATENT APPLICATION: US/09/596,444
 TIME: 14:32:02

Input Set : A:\Sequence Listing.txt.txt
Output Set: N:\CRF3\10242001\1596444.raw

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VERIFICATION SUMMARYPATENT APPLICATION: US/09/596,444

TIME: 14:32:02

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Output Set: N:\CRF3\10242001\I596444.raw

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L:849 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: